

OIPE

RAW SEQUENCE LISTING

DATE: 01/04/2002

PATENT APPLICATION: US/09/832,292

TIME: 15:12:11

Input Set : A:\ES.txt

Output Set: N:\CRF3\01042002\I832292.raw

p.5

13 <110> APPLICANT: Ryazanov, Alexey
 25 <120> TITLE OF INVENTION: MAMMALIAN ALPHA-KINASE PROTEINS, NUCLEIC ACIDS AND
 27 DIAGNOSTIC AND THERAPEUTIC USES THEREOF
 39 <130> FILE REFERENCE: 601-1-098CIP
 51 <140> CURRENT APPLICATION NUMBER: 09/832,292
 57 <141> CURRENT FILING DATE: 2001-04-10
 69 <150> PRIOR APPLICATION NUMBER: 09/632,131
 75 <151> PRIOR FILING DATE: 2001-08-03
 87 <160> NUMBER OF SEQ ID NOS: 45
 99 <170> SOFTWARE: PatentIn version 3.1
 111 <210> SEQ ID NO: 1
 117 <211> LENGTH: 238
 123 <212> TYPE: PRT
 129 <213> ORGANISM: Homo sapiens
 141 <400> SEQUENCE: 1
 149 Gly Glu Trp Leu Asp Asp Glu Val Leu Ile Lys Met Ala Ser Gln Pro
 153 1 5 10 15
 165 Phe Gly Arg Gly Ala Met Arg Glu Cys Phe Arg Thr Lys Lys Leu Ser
 169 20 25 30
 181 Asn Phe Leu His Ala Gln Gln Trp Lys Gly Ala Ser Asn Tyr Val Ala
 185 35 40 45
 197 Lys Arg Tyr Ile Glu Pro Val Asn Arg Asp Val Tyr Phe Glu Asp Val
 201 50 55 60
 213 Arg Leu Gln Met Glu Ala Lys Leu Trp Gly Asp Asp Tyr Asn Arg His
 217 65 70 75 80
 229 Lys Pro Pro Lys Gln Val Asp Ile Met Gln Met Cys Ile Ile Glu Leu
 233 85 90 95
 245 Lys Asp Arg Pro Gly Lys Pro Leu Phe His Leu Asp His Tyr Ile Asp
 249 100 105 110
 261 Gly Lys Tyr Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Arg Asp Asp
 265 115 120 125
 277 Asn Ile Arg Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg
 281 130 135 140
 293 Ser Gly His Gln Leu Ile Val Val Asp Ile Gln Gly Val Gly Asp Leu
 297 145 150 155 160
 309 Tyr Thr Asp Pro Gln Ile His Thr Glu Thr Gly Thr Asp Phe Gly Asn
 313 165 170 175
 325 Gly Asn Leu Gly Val Arg Gly Met Ala Leu Phe Phe Tyr Ser His Ala
 329 180 185 190
 341 Cys Asn Arg Ile Cys Glu Ser Met Gly Leu Ala Pro Phe Asp Leu Ser
 345 195 200 205
 357 Pro Arg Glu Arg Asp Ala Val Asn Gln Asn Thr Lys Leu Leu Gln Ser
 361 210 215 220
 373 Ala Lys Thr Ile Leu Arg Gly Thr Asp Asp Lys Cys Gly Ser
 377 225 230 235
 389 <210> SEQ ID NO: 2
 395 <211> LENGTH: 233

ENTERED

#10

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401 <212> TYPE: PRT
407 <213> ORGANISM: C. elegans
419 <400> SEQUENCE: 2
427 Leu Gln Trp Thr Glu Asp Ile Val Asp Val Arg Leu His Pro Asp Ser
431 1 5 10 15
443 Phe Ala Arg Gly Ala Met Arg Glu Cys Tyr Arg Leu Lys Lys Cys Ser
447 20 25 30
459 Lys His Gly Thr Ser Gln Asp Trp Ser Ser Asn Tyr Val Ala Lys Arg
463 35 40 45
475 Tyr Ile Cys Gln Val Asp Arg Arg Val Leu Phe Asp Asp Val Arg Leu
479 50 55 60
491 Gln Met Asp Ala Lys Leu Trp Ala Glu Glu Tyr Asn Arg Tyr Asn Pro
495 65 70 75 80
507 Pro Lys Lys Ile Asp Ile Val Gln Met Cys Val Ile Glu Met Ile Asp
511 85 90 95
523 Val Lys Gly Ser Pro Leu Tyr His Leu Glu His Phe Ile Glu Gly Lys
527 100 105 110
539 Tyr Ile Lys Tyr Asn Ser Asn Ser Gly Phe Val Ser Asn Ala Ala Arg
543 115 120 125
555 Leu Thr Pro Gln Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His
559 130 135 140
571 Gln Met Met Val Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp
575 145 150 155 160
587 Pro Gln Ile His Thr Val Val Gly Thr Asp Tyr Gly Asp Gly Asn Leu
591 165 170 175
603 Gly Ile Arg Gly Met Ala Leu Phe Phe His Ser His Arg Cys Asn Asp
607 180 185 190
619 Ile Cys Glu Thr Met Asp Leu Ser Asn Phe Glu Leu Ser Pro Pro Glu
623 195 200 205
635 Ile Glu Ala Thr Glu Val Ala Met Glu Val Ala Ala Lys Gln Lys Lys
639 210 215 220
651 Ser Cys Ile Val Pro Pro Thr Val Phe
655 225 230
667 <210> SEQ ID NO: 3
673 <211> LENGTH: 259
679 <212> TYPE: PRT
685 <213> ORGANISM: Dictyostelium discoideum
697 <400> SEQUENCE: 3
705 Asn Lys Trp Ile Arg Leu Ser Met Lys Leu Lys Val Glu Arg Lys Pro
709 1 5 10 15
721 Phe Ala Glu Gly Ala Leu Arg Glu Ala Tyr His Thr Val Ser Leu Gly
725 20 25 30
737 Val Gly Thr Asp Glu Asn Tyr Asp Pro Leu Gly Thr Thr Thr Lys Leu
741 35 40 45
753 Phe Pro Pro Ile Glu Met Ile Ser Pro Ile Ser Lys Asn Asn Gly Ala
757 50 55 60
769 Met Thr Gln Leu Lys Asn Gly Thr Lys Phe Val Leu Lys Leu Tyr Lys
773 65 70 75 80
785 Lys Glu Ala Glu Gln Gln Ala Ser Arg Glu Leu Tyr Phe Glu Asp Val

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789          85          90          95
801 Lys Met Gln Met Val Cys Arg Asp Trp Gly Asn Lys Phe Asn Gln Lys
805          100          105          110
817 Lys Pro Pro Lys Lys Ile Glu Phe Leu Met Ser Trp Val Val Glu Leu
821          115          120          125
833 Ile Asp Arg Ser Pro Ser Ser Asn Gly Gln Pro Ile Leu Cys Ser Ile
837          130          135          140
849 Glu Pro Leu Leu Val Gly Glu Phe Lys Lys Asn Asn Ser Asn Tyr Gly
853 145          150          155          160
865 Ala Val Leu Thr Asn Arg Ser Thr Pro Gln Ala Phe Ser His Phe Thr
869          165          170          175
881 Tyr Gly Leu Ser Asn Lys Gln Met Ile Val Val Asp Ile Gln Gly Val
885          180          185          190
897 Asp Asp Leu Tyr Thr Asp Pro Gln Ile His Thr Pro Asp Gly Lys Gly
901          195          200          205
913 Phe Gly Leu Gly Asn Leu Gly Lys Ala Gly Ile Asn Lys Phe Ile Thr
917          210          215          220
929 Thr His Lys Cys Asn Ala Val Cys Ala Leu Leu Asp Leu Asp Val Lys
933 225          230          235          240
945 Leu Gly Gly Val Leu Ser Gly Asn Asn Lys Lys Gln Leu Gln Gln Gly
949          245          250          255
961 Thr Met Val
977 <210> SEQ ID NO: 4
983 <211> LENGTH: 212
989 <212> TYPE: PRT
995 <213> ORGANISM: Dictyostelium discoideum
1007 <400> SEQUENCE: 4
1015 Ala Gln Trp Thr Cys Thr Ala Thr Leu Val Lys Val Glu Pro Val Pro
1019 1.          5          10          15
1031 Phe Ala Glu Gly Ala Phe Arg Lys Ala Tyr His Thr Leu Asp Leu Ser
1035          20          25          30
1047 Lys Ser Gly Ala Ser Gly Arg Tyr Val Ser Lys Ile Gly Lys Lys Pro
1051          35          40          45
1063 Thr Pro Arg Pro Ser Tyr Phe Glu Asp Val Lys Met Gln Met Ile Ala
1067          50          55          60
1079 Lys Lys Trp Ala Asp Lys Tyr Asn Ser Phe Lys Pro Pro Lys Lys Ile
1083 65          70          75          80
1095 Glu Phe Leu Gln Ser Cys Val Leu Glu Phe Val Asp Arg Thr Ser Ser
1099          85          90          95
1111 Asp Leu Ile Cys Gly Ala Glu Pro Tyr Val Glu Gly Gln Tyr Arg Lys
1115          100          105          110
1127 Tyr Asn Asn Asn Ser Gly Phe Val Ser Asn Asp Glu Arg Asn Thr Pro
1131          115          120          125
1143 Gln Ser Phe Ser His Phe Thr Tyr Glu His Ser Asn His Gln Leu Leu
1147          130          135          140
1159 Ile Ile Asp Ile Gln Gly Val Gly Asp His Tyr Thr Asp Pro Gln Ile
1163 145          150          155          160
1175 His Thr Tyr Asp Gly Val Gly Phe Gly Ile Gly Asn Leu Gly Gln Lys
1179          165          170          175

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```

1191 Gly Phe Glu Lys Phe Leu Asp Thr His Lys Cys Asn Ala Ile Cys Gln
1195          180          185          190
1207 Tyr Leu Asn Leu Gln Ser Ile Asn Pro Lys Ser Glu Lys Ser Asp Cys
1211          195          200          205
1223 Gly Thr Val Pro
1227          210
1239 <210> SEQ ID NO: 5
1245 <211> LENGTH: 2178
1251 <212> TYPE: DNA
1257 <213> ORGANISM: Homo sapiens
1269 <400> SEQUENCE: 5
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1281 gctggccatg atggtgattc tgatggggac agcgacgatg aggaaggtta cttcatctgc      120
1289 cccatcacgg atgacctcaag ctccaaccag aatgtcaatt ccaagggtta taagtactac      180
1297 agcaacctaa caaaaagtga gcggtatagc tccagcgggt ccccggaaca ctcttccac      240
1305 ttcaaggaag cctggaagca cgcaatccag aaggccaagc acatgcccga cccctgggct      300
1313 gagttccacc tggaagatat tgccaccgaa cgtgctactc gacacaggta caacgccgtc      360
1321 accggggaat ggctggatga tgaagttctg atcaagatgg catctcagcc cttcggccga      420
1329 ggagcaatga gggagtgtt ccggacgaag aagctctcca acttcttgca tgcccagcag      480
1337 tggaagggcg cctccaacta cgtggcgaag cgctacatcg agcccgtaga ccgggatgtg      540
1345 tactttgagg acgtgcgtct acagatggag gccaagctct ggggggagga gtataatcgg      600
1353 cacaagcccc ccaagcaggt ggacatcatg cagatgtgca tcatcgagct gaaggacaga      660
1361 ccgggcaagc ccctcttcca cctggagcac tacatcgagg gcaagtacat caagtacaac      720
1369 tccaactctg gctttgtccg tgatgacaac atccgactga cgccgcaggc cttcagccac      780
1377 ttactttttg agcgttccgg ccatcagctg atagtgggtg acatccaggg agttggggat      840
1385 ctctacactg acccacagat ccacacggag acgggcaactg actttggaga cggcaaccta      900
1393 ggtgtccgcg ggatggcgct cttcttctac tctcatgcct gcaaccggat ttgcgagagc      960
1401 atgggccttg ctccctttga cctctcgccc cgggagaggg atgcagtga tcagaacacc      1020
1409 aagctgctgc aatcagccaa gaccatcttg agaggaacag aggaaaaatg tgggagcccc      1080
1417 cgagtaagga ccctctctgg gagccggcca cccctgctcc gtccccttcc agagaactct      1140
1425 ggagacgaga acatgagcga cgtgaccttc gactctctcc cttcttcccc atcttcggcc      1200
1433 acaccacaca gccagaagct agaccacctc cattggccag tgttcagtga cctcgataac      1260
1441 atggcatcca gagaccatga tcatctagac aaccaccggg agtctgagaa tagtggggac      1320
1449 agcggatacc ccagtgagaa gcgggggtgag ctggatgacc ctgagccccg agaacatggc      1380
1457 cactcataca gtaatcgga gtacgagtct gacgaagaca gcctgggcag ctctggacgg      1440
1465 gtatgtgtag agaagtggaa tctcctcaac tcctcccgcc tccacctgcc gagggcttcg      1500
1473 gccgtggccc tggaagtgca aaggcttaat gctctggacc tcgaaaagaa aatcgggaag      1560
1481 tccatttttg ggaaggtcca tctggccatg gtgcgctacc acgaggggtg gcgcttctgc      1620
1489 gagaagggcg aggagtggga ccaggagtcg gctgtcttcc acctggagca cgcagccaac      1680
1497 ctgggcgagc tggaggccat cgtgggcctg ggactcatgt actcgagtt gcctcatcac      1740
1505 atcctagccg atgtctctct gaaggagaca gaagagaaca aaaccaaagg atttgattac      1800
1513 ttactaaagg ccgctgaagc tggcgacagg cagtccatga tcctagtggc gcgagctttt      1860
1521 gactctggcc agaacctcag cccggacagg tgccaagact ggctagaggc cctgcactgg      1920
1529 tacaacactg ccctggagat gacggactgt gatgagggcg gtgagtacga cggaatgcag      1980
1537 gacgagcccc ggtacatgat gctggccagg gaggcagaga tgctgttcac aggaggctac      2040
1545 gggctggaga aggacctgca gagatcaggg gacttgata cccaggcagc agaggcagcg      2100
1553 atggaagcca tgaagggccg actggccaac cagtactacc aaaaggctga agaggcctgg      2160
1561 gccagatgg aggaataa
1573 <210> SEQ ID NO: 6

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1579 <211> LENGTH: 724

1585 <212> TYPE: PRT

1591 <213> ORGANISM: Homo sapiens

1603 <400> SEQUENCE: 6

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1611 Met Ala Asp Glu Asp Leu Ile Phe Arg Leu Glu Gly Val Asp Gly Gly
1615 1          5          10          15
1627 Gln Ser Pro Arg Ala Gly His Asp Gly Asp Ser Asp Gly Asp Ser Asp
1631          20          25          30
1643 Asp Glu Glu Gly Tyr Phe Ile Cys Pro Ile Thr Asp Asp Pro Ser Ser
1647          35          40          45
1659 Asn Gln Asn Val Asn Ser Lys Val Asn Lys Tyr Tyr Ser Asn Leu Thr
1663          50          55          60
1675 Lys Ser Glu Arg Tyr Ser Ser Ser Gly Ser Pro Ala Asn Ser Phe His
1679 65          70          75          80
1691 Phe Lys Glu Ala Asn Lys His Ala Ile Gln Lys Ala Lys His Met Pro
1695          85          90          95
1707 Asp Pro Trp Ala Glu Phe His Leu Glu Asp Ile Ala Thr Glu Arg Ala
1711          100         105         110
1723 Thr Arg His Arg Tyr Asn Ala Val Thr Gly Glu Trp Leu Asp Asp Glu
1727          115         120         125
1739 Val Leu Ile Lys Met Ala Ser Gln Pro Phe Gly Arg Gly Ala Met Arg
1743          130         135         140
1755 Glu Cys Phe Arg Thr Lys Lys Leu Ser Asn Phe Leu His Ala Gln Gln
1759 145         150         155         160
1771 Trp Lys Gly Ala Ser Asn Tyr Val Ala Lys Arg Tyr Ile Glu Pro Val
1775          165         170         175
1787 Asp Arg Asp Val Tyr Phe Glu Asp Val Arg Leu Gln Met Glu Ala Lys
1791          180         185         190
1803 Leu Trp Gly Glu Glu Tyr Asn Arg His Lys Pro Pro Lys Gln Val Asp
1807          195         200         205
1819 Ile Met Gln Met Cys Ile Ile Glu Leu Lys Asp Arg Pro Gly Lys Pro
1823          210         215         220
1835 Leu Phe His Leu Glu His Tyr Ile Glu Gly Lys Tyr Ile Lys Tyr Asn
1839 225         230         235         240
1851 Ser Asn Ser Gly Phe Val Arg Asp Asp Asn Ile Arg Leu Thr Pro Gln
1855          245         250         255
1867 Ala Phe Ser His Phe Thr Phe Glu Arg Ser Gly His Gln Leu Ile Val
1871          260         265         270
1883 Val Asp Ile Gln Gly Val Gly Asp Leu Tyr Thr Asp Pro Gln Ile His
1887          275         280         285
1899 Thr Glu Thr Gly Thr Asp Phe Gly Asp Gly Asn Leu Gly Val Arg Gly
1903          290         295         300
1915 Met Ala Leu Phe Phe Tyr Ser His Ala Cys Asn Arg Ile Cys Glu Ser
1919 305         310         315         320
1931 Met Gly Leu Ala Pro Phe Asp Leu Ser Pro Arg Glu Arg Asp Ala Val
1935          325         330         335
1947 Asn Gln Asn Thr Lys Leu Leu Gln Ser Ala Lys Thr Ile Leu Arg Gly
1951          340         345         350
1963 Thr Glu Glu Lys Cys Gly Ser Pro Arg Val Arg Thr Leu Ser Gly Ser

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/832,292

DATE: 01/04/2002

TIME: 15:12:12

Input Set : A:\ES.txt

Output Set: N:\CRF3\01042002\I832292.raw

L:7559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16
L:8007 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:8323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18
L:8603 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:8767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22